Amendments to the Claims:

This listing of claims will replace all prior versions and listings of the claims in this application:

1-44. (Canceled)

45. (new) An isolated nucleic acid encoding a mutant type 2 metabotropic glutamate receptor (mutant mGluR2) comprising an amino acid sequence selected from the group consisting of SEQ.ID.NOS.: 1 - 8.

46. (new) An isolated nucleic acid molecule of claim 45 comprising a nucleotide sequence selected from the group consisting of SEQ.ID.NOS.: 9 - 16.

47. (new) An isolated nucleic acid containing a sequence encoding a mutant mGluR2 of claim 45, wherein the isolated nucleic acid sequence is selected from the group consisting of:

(a) SEQ.ID.NOS.: 9 - 16;

(b) a nucleic acid sequence complementary to any sequence of (a); and

(c) a fragment of (a) or (b) that is at least 144 base pairs in length which will selectively hybridize to human genomic DNA encoding a human metabotropic glutamate receptor and which will encode the sequence of a mutant mGluR2 comprising at least one amino acid substitution at position 688, 689 or 735 of a wild-type type 2 metabotropic glutamate receptor (wild-type mGluR2).

48. (new) An expression vector comprising the nucleic acid of claim 46 in combination with regulatory elements necessary for expression of the nucleic acid in a suitable host cell.

49. (new) An expression vector of claim 48, wherein the host cell is of mammalian origin.

50. (new) A method for producing a mutant mGluR2 of claim 45 comprising the steps of:

(a) expressing a nucleic acid molecule comprising a nucleotide sequence that encodes a recombinant mutant mGluR2 protein comprising an amino acid sequence selected from the group consisting of SEQ.ID.NOS.: 1 - 8 in a suitable host cell under conditions favoring expression of the recombinant mutant mGluR2 protein; and

(b) purifying the recombinant mutant mGluR2 protein by any suitable method.

51. (new) An isolated mutant mGluR2 wherein the mutant mGluR2 is characterized as being capable of depotentiating glutamate receptor activity relative to wild-type mGluR2.

52. (new) A mutant mGluR2 of claim 51 comprising wild-type mGluR2 having at least one amino acid substitution at an amino acid position within the wild-type mGluR2 amino acid sequence sufficient to enable the mutant mGluR2 to depotentiate glutamate receptor activity by altering an allosteric site associated with transmembrane region 4 or 5 of the mGluR2 relative to wild-type mGluR2.

53. (new) A mutant mGluR2 of claim 52, wherein the amino acid substitution comprises a substitution of leucine for serine at position 688 (S688L) of wild-type mGluR2 (SEQ.ID.NO.: 4).

54. (new) A mutant mGluR2 of claim 52, wherein the amino acid substitution comprises a substitution of valine for glycine at position 689 (G689V) of wild-type mGluR2 (SEQ.ID.NO.: 7).

55. (new) A mutant mGluR2 of claim 52, wherein the amino acid substitution comprises substitution of aspartic acid for asparagine at position 735 (N735D) of wild-type mGluR2 (SEQ.ID.NO.: 1).

56. (new) A mutant mGluR2 of claim 52, wherein the amino acid substitution comprises substitution of:

(a) leucine for serine at position 688 (S688L); and

(b) aspartic acid for asparagine at position 735 (N735D)

of wild-type mGluR2 (SEQ.ID.NO.: 6).

57. (new) A mutant mGluR2 of claim 52, wherein the amino acid substitution comprises substitution of:

(a) valine for glycine at position 689 (G689V); and

(b) aspartic acid for asparagine at position 735 (N735D)

of wild-type mGluR2 (SEQ.ID.NO.: 2).

58. (new) A mutant mGluR2 of claim 52, wherein the amino acid substitution comprises substitution of:

leucine for serine at position 688 (S688L);
valine for glycine at position 689 (G689V); and
aspartic acid for asparagine at position 735 (N735D)
of wild-type mGluR2 (SEQ.ID.NO.: 3).

59. (new) A mutant mGluR2 of claim 52, wherein the amino acid substitution comprises a substitution of:

(a) leucine for serine at position 688 (S688L); and

(b) aspartic acid for asparagine at position 735 (N735D)
of wild-type mGluR2 (SEQ.ID.NO.: 6).

60. (new) A mutant form mGluR2 of claim 51, wherein the amino acid substitution comprises a substitution of:

leucine for serine at position 688 (S688L);
valine for glycine at position 689 (G689V);
threonine for alanine at position 733 (A733T); and
aspartic acid for asparagine at position 735 (N735D)
of wild-type mGluR2 (SEQ.ID.NO.: 8).

61. (new) A mutant type 3 metabotropic glutamate receptor protein (mutant mGluR3) wherein the mutant mGluR3 is characterized as being capable of depotentiating glutamate receptor activity relative to a wild-type type 3 metabotropic glutamate receptor (wild-type mGluR3).

62. (new) A mutant mGluR3 of claim 61 comprising wild-type mGluR3 having at least one amino acid substitution at a position within the wild-type mGluR3 amino acid sequence sufficient to enable the mutant mGluR3 to depotentiate glutamate receptor activity by altering an allosteric site associated with transmembrane region 4 or 5 of the mutant mGluR3 relative to wild-type mGluR3.

63. (new) A mutant mGluR3 of claim 62, wherein the amino acid substitution comprises a substitution of valine for glycine at position 698 (V698G) of wild-type mGluR3 (SEQ.ID.NO.: 39).

64. (new) A mutant mGluR3 of claim 62, wherein the amino acid substitution comprises a substitution of:

serine for leucine at position 697 (L697S); and

asparagine for aspartic acid at position 744 (D744N)

of wild-type mGluR3 (SEQ.ID.NO.: 38).

65. (new) A mutant mGluR3 of claim 62, wherein the amino acid substitution comprises a substitution of:

glycine for valine at position 698 (V698G); and

asparagine for aspartic acid at position 744 (D744N)

of wild-type mGluR3 (SEQ.ID.NO.: 34).

66. (new) A mutant mGluR3 of claim 62, wherein the amino acid substitution comprises a substitution of:

serine for leucine at position 697 (L697S);

glycine for valine at position 698 (V698G); and

asparagine for aspartic acid at position 744 (D744N)

of wild-type mGluR3 (SEQ.ID.NO.: 35).

67. (new) A mutant mGluR3 of claim 62, wherein the amino acid substitution comprises a substitution of:

serine for leucine at position 697 (L697S); and

glycine for valine at position 698 (V698G)

of wild-type mGluR3 (SEQ.ID.NO.: 37).

68. (new) A mutant receptor mGluR3 of claim 62, wherein the amino acid substitution comprises a substitution of:

serine for leucine at position 697 (L697S);

glycine for valine at position 698 (V698G);

alanine for threonine at position 742 (T742A); and

asparagine for aspartic acid at position 744 (D744N)

of wild-type mGluR3 (SEQ.ID.NO.: 40).

69. (new) A mutant mGluR3 of claim 62 wherein the amino acid substitution comprises a substitution of serine for leucine at position 697 (L697S) of wild-type mGluR3 (SEQ.ID.NO.:36).